

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.825. Applicant's attention is directed to these regulations, published at 1114 May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure or paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7.

Other: _____

Applicant must provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☐ An ~~initial~~ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☐ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/813,781

TEAM 8

DATE: 04/18/97

TIME: 15:53:16

INPUT SET: S17080.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information

GENERAL INFORMATION: all listings
are in
upper-case
letters

(i) APPLICANT: Weidanz, Jon A.
Card, Kimberlyn F.
Wong, Hing C.

(ii) TITLE OF ~~THE~~ INVENTION: FUSION PROTEINS COMPRISING
BACTERIOPHAGE COAT PROTEIN

(iii) NUMBER OF SEQUENCES: 130

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
(B) STREET: 130 Water Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: RESNICK, DAVID S
(B) REGISTRATION NUMBER: 34,235
(C) REFERENCE/DOCKET NUMBER: 46745

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617 523 3400

INPUT SET: S17080.raw

46 (B) TELEFAX: 617 523 6443
47 (C) TELEX:
48
49

ERRORED SEQUENCES FOLLOW:

828 (2) INFORMATION FOR SEQ ID NO:44:
829
830 (i) SEQUENCE CHARACTERISTICS:
--> 831 (A) LENGTH: 35 base pairs 28 shown
832 (B) TYPE: nucleic acid
833 (C) STRANDEDNESS: single
834 (D) TOPOLOGY: linear
835
836 (ii) MOLECULE TYPE: cDNA
837 (iii) HYPOTHETICAL: NO
838 (iv) ANTI-SENSE: NO
839 (v) FRAGMENT TYPE:
840 (vi) ORIGINAL SOURCE:
841
842 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
843
--> 844 CCGGGTCATC AGTGATGATG GTGAGCG G
845

(35) 28

1868 (2) INFORMATION FOR SEQ ID NO:101:
1869
1870 (i) SEQUENCE CHARACTERISTICS:
--> 1871 (A) LENGTH: 30 base pairs 29 shown
1872 (B) TYPE: nucleic acid
1873 (C) STRANDEDNESS: single
1874 (D) TOPOLOGY: linear
1875
1876 (ii) MOLECULE TYPE: cDNA
1877 (iii) HYPOTHETICAL: NO
1878 (iv) ANTI-SENSE: NO
1879 (v) FRAGMENT TYPE:
1880 (vi) ORIGINAL SOURCE:
1881
1882 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
1883
--> 1884 GCCGGCCATG GCCRGTGCTG TCRTCTCTC
1885 "group 9"

(30) 29

2192 (2) INFORMATION FOR SEQ ID NO:119:
2193
2194 (i) SEQUENCE CHARACTERISTICS:
--> 2195 (A) LENGTH: 33 base pairs 32 shown
2196 (B) TYPE: nucleic acid

See next page

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/813,781DATE: 04/18/97
TIME: 15:53:22

INPUT SET: S17080.raw

2197 (C) STRANDEDNESS: single
2198 (D) TOPOLOGY: linear
2199
2200 (ii) MOLECULE TYPE: cDNA
2201 (iii) HYPOTHETICAL: NO
2202 (iv) ANTI-SENSE: NO
2203 (v) FRAGMENT TYPE:
2204 (vi) ORIGINAL SOURCE:
2205
2206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
2207

--> 2208 GGAGGCGGCG GTTCTCAGAG AGTGACTCA GCC
2209

group of 9

33

32

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/813,781DATE: 04/18/97
TIME: 15:53:33

INPUT SET: S17080.raw

Line	Error	Original Text
831	Entered (35) and Calc. Seq. Length (28) differ	(A) LENGTH: 35 base pairs
844	# of Sequences for line conflicts w/ running total	CCGGGTCATC AGTGATGATG GTGAGCG G
1871	Entered (30) and Calc. Seq. Length (29) differ	(A) LENGTH: 30 base pairs
1884	# of Sequences for line conflicts w/ running total	GCCGGCCATG GCCRG TGCTG TCRTCTCTC
2195	Entered (33) and Calc. Seq. Length (32) differ	(A) LENGTH: 33 base pairs
2208	# of Sequences for line conflicts w/ running total	GGAGGCGCGG GTTCTCAGAG AGTGACTCA GCC